

1/48

FIGURE 1

200KD -100.5KD -72KD -43KD -28.5KD -

> 1 - anti- EGFr PoAB RK-2 2 - Cyt-356 MoAB/RAM 3 - RAM

FIGURE 2A

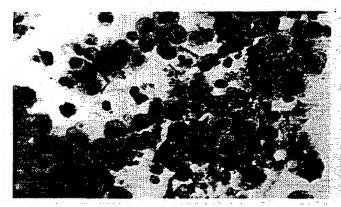


FIGURE 2B

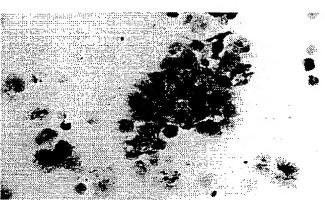


FIGURE 2C

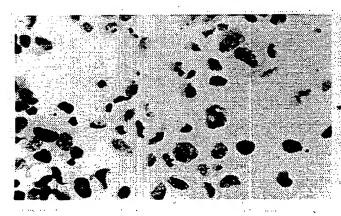


FIGURE 2D

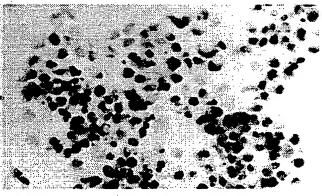


FIGURE 3A

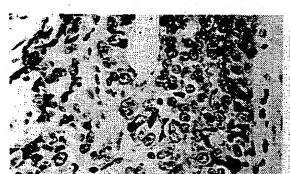


FIGURE 3B

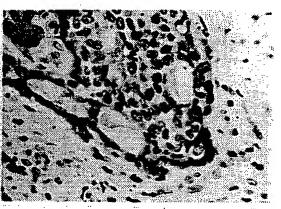
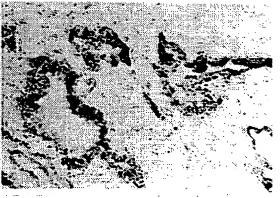


FIGURE 3C



FIGURE 3D



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FIGURE 4

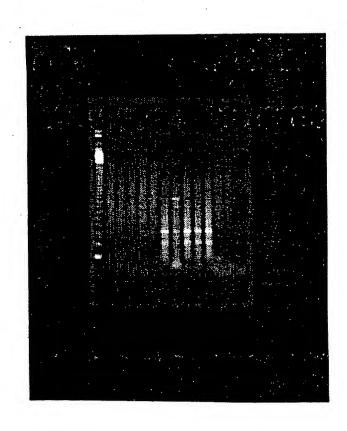
100.5

72.0

43.0

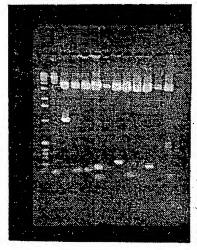
28.5

5/48 FIGURE 5



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FIGURE 6A FIGURE 6B



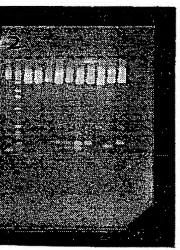


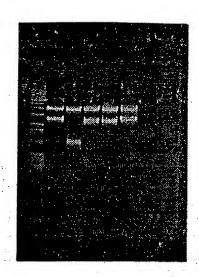
FIGURE 7

6.1KB →

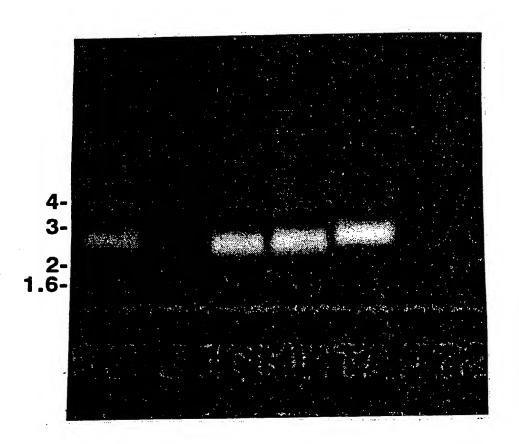
0.5KB -

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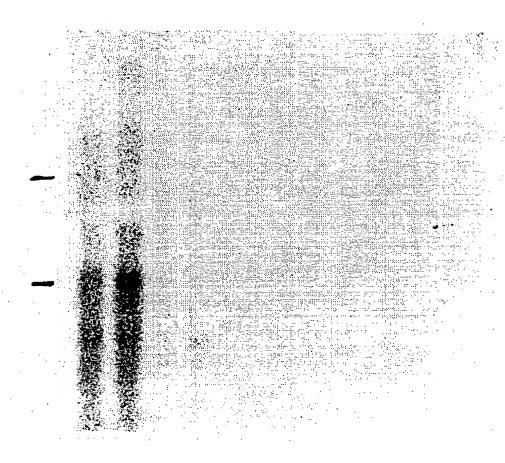
FIGURE 8



9/48 FIGURE 9



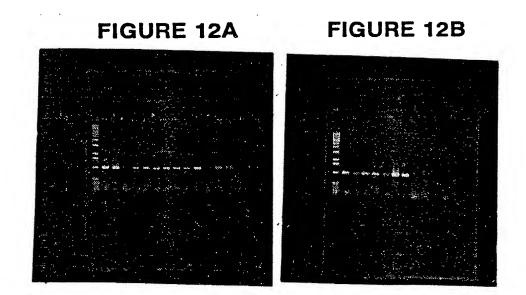
10/48 FIGURE 10



11/48 FIGURE 11

1 2 3 9.5___ 7.5__ 4.4__ 2.4__

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13/48 FIGURE 13

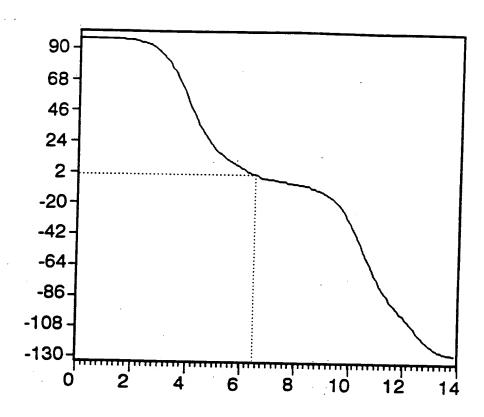


FIGURE 14-1

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

8 4 10 **^**| **^**II î Â A AA AA 309 264 9/ 101 CNAT CNAT CNAT -88 0 II 11 II conformation conformation conformation conformation EEC EEC Extended Helical Turn Coil

14/48

Sequence shown with conformation codes.

given conformation are Ø in or more residues Ŋ Consecutive stretch of overlined

|田 IH IH 163 II H IH 161 IX H 回 H 10 नि IH 10 161 II 10 田田 IH H 10 田 10 F IH **[E**] 回 IH नि IH 臼 H 田 10 H 田 10 H 臼 IU H 回 IU 闰 臼 H IU 闰 10 H 田 II IH IH IH 二 II 田 IH II II IH IH II IH 王 IX IH IX II IX 田 IH II 田 二 田 IH 田 IH **|**臼 二 H 田 二二 田 IH 31 61

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मि	ပ	FI	旧	 四	ပ	巨	 回	नि	H	旧	回	ı
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	H	旧	回	 四	E	旧	回	E	म	E	IH	ı
IH	চি	नि	E	H	H	नि	lEI	धि	ध्य	ບ	IH	ı
II	回	धि	IEI	E	回	E	E	मि	E	ပ	IH	1
IH	मि	ပ	E	回	াচন	ပ	团	ွပ	ध	Ö	IH	1
三王	नि	ပ	IEI	E	E	ပ	H	ပ	E	E	IH	ı
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IH	ပ	ပ	H	回	田	E	E	阳	ပ	ပ	Œ	1
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ल	巨	लि	II	III	H	阳	E	II	 匝	II	Ö	1
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91	121	151	181	211	241	271	301	331	361	391	421	

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H	旧	ध	田田	II	E	国	मि	1=	133
H	田	E	田田	E	旧	ပ	回	II	II
H	IEI	H	IH	田	ि	ပ	回	IH	IH
H	H	त्र	II	लि	回	E	E	IH	IH
H	IO	ल	IH	ि	回	Ħ	ाध्य	II	IH
H	10	E		मि	H	E	H	II	IH
臼	10	ပ	II	旧	IH	ΙΞ	ပ	IH	IX
团	IO	ပ	III	旧	IH	IH	ပ	IH	II
田	O	ပ	川田	II	IH	II	ပ	IH	IH
臼	H	H	II	IH	IH	II	H	E	IX
臼	H	II	II	III	Ö	III	H	臼	IH
臼	H	II	IX	II	Ö	II	回	H	नि
团	H	H	旧	IX	Ħ	IΞ	闰	回	E
臼	IH	IH	E	回	मि	II	H	IEI	नि
田	IH	II	巨	lei	回	III ·	IH	旧	回
回	IH	回	E	巨	EI	II	H	E	回
田	IH	田	IE	巨	i田	II	Œ	阳	回
回	IH	田	田	巨	国	IH	II	IEI	IFI
臼	IH	IO	lei	巨	H	II	II	E	回
H	王	, IO	E	田	H	IH	II	Ö	IH
H	I	D	Ö	田	IH	IX	IH	Ö	IH
团	II	10	. 164	E	IH	IH	II	Ö	IH
团	II			Ħ	IH	ı	IH	ပ	IH
Ö	I		IE	円	IH	IH	IX	H	IH
r U	II		IE	IH	IH	江	II	लि	IX
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[F]	O '	ि	[2]	IH	Œ	IX	ाध	धि	IH
দা	III ·	E	H	III	II	H	回	回	ပ
451	481	511	541	571	601	631	199	691	721

FIGURE 14-4

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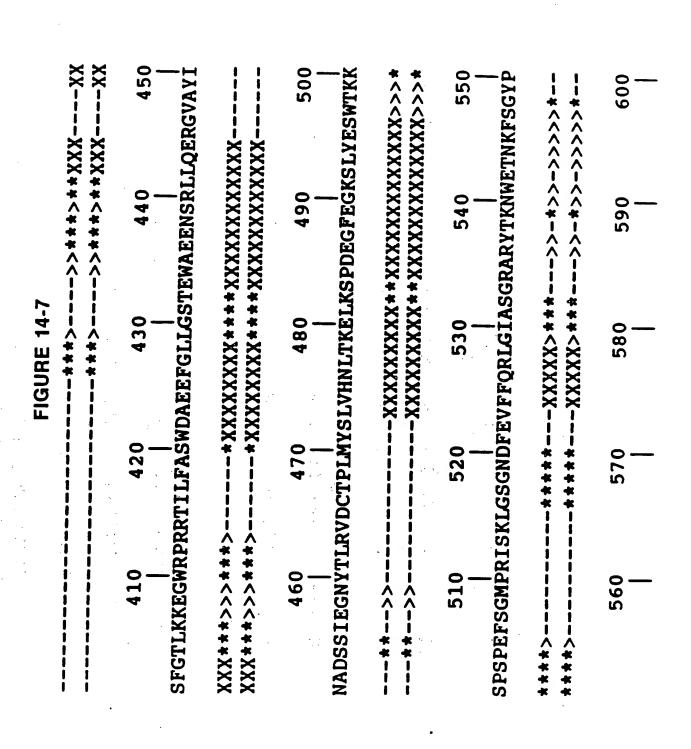
Conformation: > 10	Helical	conformation: X Extended conformat	conformation: X	× ••	Extended conformation:	l confor	mation:	1
30 40 	Turn	conf	ormation	< ^	coil	confor	mation: mation:	I *
CAGALVLAGGFFLLGFLFGWFIKSSN XXXXXX****** 80 90		10	20	Č ·	0	o_	50	
****XXXXX	XXXX	XXXXX	X		XXX	CWF LKSS	NEAT	
	4	60 60	70	! ! ! ! !	i i i	.***** 0	** **	

FIGURE 14-5

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150 200 KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGK1 -*X-XXXXXXXXXXXXXXXX---><---140 190 ----** XXXXXXX** * < < ----**<<<-----XXXXXXX***<<-160

230 240 AKGVILYSDPADYFAPGVKSYPDGWN X>>>>>>>>>>>>>	^			-XXXXXXXXXXXXXXXXXX-	XX>>>
X>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	210 IARYGKVFRGNK	220 VKNAQLAGAKG	230 SVILYSDPAD	240 KFAPGVKSYPI	250 DGWNLPG
280 290 	*^^	*XXXXXXXX*	·		^**-^^
->>*****X**	260 GGVQRGNILNLNG	270 AGDPLTPGYPA	280 INEYAYRGI	290 	300 VHPIGYY
330 340 *-*XXXXXXX*	^ + ·	# # # # A A A	XX	# # # 	
XXXXXX	310 AQKLLEKMGGSA	320 PPDSSWRGSLK	330 VPYNVGPGF	340 GNFSTQKVK	350 HIHSTN
370 380 390	XXXXXX->>>**	<<		-*XXXXX*-*-	* * *
	360	370	380	390	400



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>XXX 650 IASKFSERL	XXXXXXXXX	700 YAPSSHNKY	***\\	750 AAETLSEVA	-XXXXXXXXXXXXX-
XXXXX- 640 	XXXXXXXXX	690 PDRPFYRHVI		740 YVAAFTVQA	XXXX
XX-X 630 		680 RAFIDPLGL	XXX>>**	730 KAWGEVKRQ]	XXXXXXX
KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	X**XXXX	670 	-xxxxxxxxx	720 FDIESKVDPS	-XXXXXXXX****XXXXXXX-
XXXXXXX 610 AVVLRKYADKIY	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	660 QDFDKSNPIVLR	XX>>>++<> <xx< td=""><td>710 AGESFPGIYDAL</td><td>XXX<</td></xx<>	710 AGESFPGIYDAL	XXX<
	XXXXXXXXXXXXX-XXXXXXX> 620 630 640	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	610 620 630 640 650 650 640 KXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	610 620 630 640 650 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

22/48 FIGURE 15A

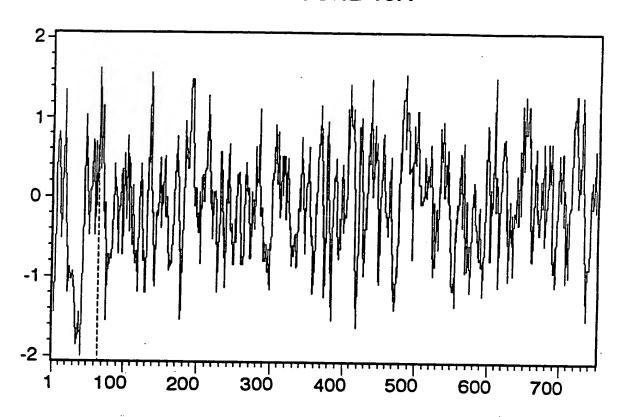


FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

-> This is the value recommended by the authors averaging group length is: 6 amino acids. The method used is that of Hopp and Woods. The

The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu 68 t From 1.62

Asn-Glu-Asp-Gly-Asn-Glu Lys-Ser-Pro-Asp-Glu-Gly 137 to 132 482 From From 1.57 1.55

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 1004 of the cases assigned to a known antigenic group. The second and third point: of incorrect predictions. proportion of 33% gave a

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opt	321	311	266	321				
t1	120	164	145	120 3	1020 1030 1040 1050 1060 1070 TGTCCAGCGTGGAATATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA	CHKTFE TACACTTATCCCATTCGGACATGCCCACCTTGGAACTGGAGACCCTTACACCCCAGGCTT 990 1000 1010 1020 1030 1040	1080 1090 1100 1110 1120 1130 CCCAGCAAATGAATAGCCTTATAGGCGTGGAATTGCAGGGCTGTTGGTCTTCCAAGTAT ::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 1190 TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTC :::::::::::::::::::::::::::::
initl		_		13	70 CCAC	CAGG 1040	30 30 30 30 30 30 30 30 30 30 30 30 30 3	36TC
initn	203	164	145	203	1050 1060 1070 IGGTGCAGGAGACCCTCTCACACCAGGTT	CACC	1130 1130 130 130 130 1080 1080 1080	1190 AAAATGGGTGG ::::::::: AAAATGGATGG
੶ਜ			Cd		PTCT.	CCTTA 1030	:: :: :AGG	AAAA :: 3CAA
			ete		1060 GACCC	10 10	1120 GCTGTTC ::	1180 CTAG! : TTCA(
	for transferrin receptor	end.	rin receptor mRNA, complete	for transferrin receptor nt overlap	1 GGAG	GGAG	1 3: 1080	1180 SAAGCTCCTAG
	rece	3,	A ,	rece	O TGCA	AACTO 1020	0 TGC? : AGT'I	OGAAC
<u>-9</u>	rin	RNA,	mRN	rin	1050 ATGGT	TTGG	GCGTGGAATTC:::::::::::::::::::::::::::::	1170 GCACAG2 ::: GCAGCC2
FIGURE 16-1	sfer	or m	ptor	sfer ap	CTGA	CACC 10	CGTGGZZ : : : : : : : : : :	TGATGC :: :: TGCAGC
<u>5</u>	tran	Rat transferrin receptor mRNA, 3' end.	ecel	for transf nt overlap	1040 TAAAT	rgcccA 1010	1100 ATAGG:::	1160 ACTAT : :
	for (re	cin 1	for t	1(BACA	CTTA	GGATA TCTAG
	•	·=	feri		ATAI	TTCG 1000	O TATGC : : CACAC	ATTG
. a	S IR	nsfe	rans	s mR in 7	1030 GGAAA	CCAT	1090 GAATZ	1150 CCAAT : ::
ั	11us	trai	in t	allu: ity	TSOS	ratc	AAAT	rcar ::: rcag
scores are:	G.dallus mRNA	Rat	Human transfer	G.gallus mRNA identity in 717	CCAC	ACTT/ 990	1080 1090 CCCAGCAAATGAATATG ::::::::::::::::::::::::::::	40 CTGTTCA:::: CTGTTCA(
	מ			id		TAC	1080 CCCAC ::: CCCT	
mho host	THE DES	RATTRER	HUMTFRR	CHKTFER 51.9%	pmsgen	TFE	pmsgen CHKTFE	pmsgen CHKTFE
4	CHR	RAT	HO	CHI	pms	CHK	pms	pms

210 1220 1230 1240 1250 ATAGCAGCTGGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG : :: :::::::::::::::::::::::::::::::	270 1280 1310 ACTITICTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT : : : : : : : : : : : : : : : : : : :	GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1390 1400 1410 1420 1430 CATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTTGACCCTCAGAGTGGAGC : ::::::::::::::::::::::::::::::::::
1220 1230 AGCTGGAGAGGAAGTCTCAAA : ::: :: :: :: :: :- :- :- :- :- :- :- :	1280 1290 rctacacaaaagrcaagarg : : : : : : : : : : : : : : : : : : :	1340 1350 TGTGATAGGTACTCTCAGAGGA : :::::::::::::::::::::::::::::::	1400 1410
1210 pmsgen AGCACCACCAGATAGC :: :: :: CHKTFE CACATGCTCTGA-AG-	1260 1270 CTTTACTGGAAACTTTT : :::: CAAAGCAGGAGAC	1320 1330 GACAAGAATTTACAATG : :: :: CAGGAAGATTCTGAACA	1380 1390 CATTCTGGGAGGTCACC : ::: :: TGTGATTGGAGCCCAGA 1330 1340
	IR) TEEHS ETUTITE BL	pmsgen CHKTFE	pmsgen CHKTFE

FIGURE 16-3

•	26/4	48	
1440 1450 1460 1470 1480 1490 AGCTGTTGTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGTGGAG :::::::::::::::::::::	1500 1510 1520 1530 1540 1550 pmsgen ACCTAGAACTTTTGTTTTGCAAGCTGGGATGCAGAAGTTTTGGTCTTCTTGGTTC ::::::::::::::::::::	1560 1570 1580 1590 1600 1610 pmsgen TACTGAGTGGCAGAGGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA :::::::::::::::::::::::::::::	1620 1640 1650 1670 TGC-TGACTCTATAGAAGGAAACTA-CACTCTGAGATTGATTGTACACCGCTGATG ::::::::::::::::::::::::::::::::::::
1440 1450 1460 1470 1480 1490 AGCTGTTGTTCATGAAATTGTGAG——GAGCTTTGGAACACTGAAAAGGAAGGTGGAG ::::::::::::::::::::::	1540 \AGAATTTGGTC ::::::::::::::::::::::::::::::::	1560 1570 1580 1590 1600 1610 TACTGAGTGGCCAGAGATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTA ::::::::::::::::::::::::::::::	AGTTGATTGTA ::::::::::::::::::::::::::::
1470 GAGCTTTGGAAC :::::: GATCTCAGACAT	1520 1530 15 TGTTTGCAAGCTGGGATGCAGAATT : X:::::::::::::::::::::::::::::::::::	1590 CTCCTTCAAGA : :: :: ::	1640 1650 GGAAACTA-CACTCTGAGA ::::::::::::::::::::::::::::::::::
1460 ATTGTGAGG ::: :::	1520 FGTTTGCAAGC X:::::::	70 1580 GGAGAATTCAAGA ::::X GGGGTACTCTGCC	D 1640 SAAGGAAACTA :::::: CCTGGGAGCAA
1450 GTTCATGAAA1 : :: : TTGTTGGAAC7	1510 AGAACAATTT ::: :: CGAAGCATCAT	1570 TGGGCAGAGG/ ::: ::: TGGCTGGAGG(0 1630 CTCATCTATAG : :: ATGCTCCAGTC
	1500 ACCTAGAAGAACA ::: :: :: ACCGAGGCGAAGC 1450 1450	1560 ::::::::::::::::::::::::::::::::::::	
pmsgen CHKTFE	pmsgen	pmsgen	pmsgen

FIGURE 16-4

	•
1730 CTTTGAAGGC :: :: :: CTCAGAGAGC	1790 SCATGCCC
1720 SATGAAGGCT : : :: CAGCAGTCT	1770 1780 CTTCCCCAGAGTTCAGTGG
1690 1700 1710 1720 1730 ACAACCTAACAAAAGCTGAAAAGCCCTGATGAAGGCTTTTGAAGGC : : : : : : : : : : : : : : : : : : :	1770 CCCTTCCCCAG
1700 PAACAAAAGAGCT(: : : : : : : : : : : : : : : : : : :	1760 CTAAAAAAAG1 : : : CCAGACTGGGT
1690 CACAACCTAA : : : GGGAGTATTA	1750 176 GAAAGTTGGACTAAAA : :::: :: CAGACTTGGCCCAGAC
1680 1690 1700 1710 1720 1730 pmsgen TACAGCTTGGTACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTTGAAGGC :::::::::::::::::::::::::::::::::	pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC ::::::::::::::::::::::::::::::::::
pmsgen CHKTFE	- Dimeden 7 CHKTFE (B) THEET (RULE 26)
SUBSTITUTE	SHEET (RULE 26)

IGURE 16-5

31	<u>-</u>	J.L.	\CT
164	TGGCT	TAGAT	10 \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
164	1250 TGTTGGACC	GTTGGAAT? 660	1310 ACTCT-ACCAA :::::::: ACTGTGAACAA
3' end.	0 1240 1250 CAAAGTGCCCTACAATGTTGGACCTGGCTT	TGTCCTCCTA 650	1300 GCACATC-CA : : : : : : : : : : : : : : : : : : :
errin receptor mRNA, 3' end 560 nt overlap	1220 1230 1240 1250 GCTGGAGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTT-	TTCAAAAACATGGAAGGAAACTGTCCTCCTAGTTGGAATATAGATTC 630 640 650	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCACTGTGAACAATGTACT 670 680 690 700 710
errin receptor 560 nt overlap	1220 GCTGGAGAGG	TTCAAAAACA 630	1280 TTCTACACAA :: GAACTTTCAC
TTRFR Rat transfers.58 identity in	1210 CCAGATAGCA	AGAAAAGCTA 620	0 1270 TACTGGAAACTT : :: :: TCATGTAAGCTG
RATTRFR 55.5% id	1210 pmsgen ccAccAGATAGCA	RATTRF TGCAGAAAAGCTA' 610 620	1260 pmsgen -TA : RATTRF CTC 670
	SUBSTITU	JTE SHEET	(RULE 26)

FIGURE 16-6

		29/	48	
1370 CAGACAG	CAGACCG	1430 CTCAGAG ::::	1480 AAAAGGAA ::::: TCAAAAGAT 00	1540 TTTGGTCTT : :: : TATGGAGCT 60
1360 AGTGGAAC	: :::::::: TGAGGAACCAGACC	1420 :TATTGACC:::::	14 CTGAA ::: ATGATTTC 900	15 GAAGAATT : :: : GGAGACTA'
1350 CAGAGGAGC	: : : :: TATTAAAGGCTA 770	1410 14 GTTTGGTGGTAT :::::: CCCTGGT-GTTG 830	1470 FTTGGAACA- ::::::::::::::::::::::::::::::::::	1530 rgggargca ::: :::: rggacrgca
1340 TAGGTACTCT	TTGGCGTTAT 760	1390 1400 1410 1420 1430 AGGTCACCGGGACTCATGGTGTTTGGTGTATTGACCCTCAGAG :: :: :: :: :: :: :: :: :: :: :: :: ::	1450 1460 1470 1480 FTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA : ::::: : :::::::::::::::::::::	1510 1520 1530 1540 AATTTTGTTTGCAAGCTGGATGCAGAAGAATTTGG :::::::::::::::::::::::::::
1330 TACAATGTGAT	TAACATCTT 750	90 1 TCACCGGGA :: ::: CCAGAGAGA 810	1450 CATGAAATTG ::::: GTTGAAACTT	1510 ACAATTTTG: : :::: AGTATTATC: 930
0 AAGAATTTA	ACAAGAATACT 740	1390 TTCTGGGAGGTC::::::::::::::::::::::::::::	40 1 CTGTTGTTC : : : GTCTT-CTG	1500 AGACCTAGAAGA/ X::::::::
1320 1330 1340 1350 1360 1370 pmsgenAAGTGACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGGAGCAGTGGAACCAGACAG	RATTRF GAAAGAAACAAGAATACTTAACTTTGGCGTTATTAAAGGCTATGAGGAACCAGACCG 730 740 750 760 770 780	13 TATGTCA :: TACATTG	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTTGTTGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA :::::::::::::::::::::::::::	1490 1500 1510 1520 1530 1540 GGGTGGAGACCTAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTTGTCTT :: X:::::::::::::::::::::::::::::::::
pmsgen	RATTRF 73			pmsgen (RATTRF
		Substitute Si	HEET (RULE 26)	

FIGURE 16-7

1550 1560 1600 pmsgen ctrggtrctactgagtggcagtagagatrcaagactrcaagagcgtggcgtg :::::::::::::::::::::::::::::	pmsgen GCTTATATTAATGCTGACTCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTAC ::::::::::::::::::::::::::::::::::::	pmsgen ACCGCTGATGTACAGCTTGGTACCAACCTAACAAAGAGCTGAAAAGC-CCTGATGAAG :::::::::::::::::::::::::::::::
1580 ATTCAAGACT X :::: ACCTTTCATCTTT 1000	1640 AAGGAAACTA-CA :: ::::: CTGGGTACTAGCA	1690 1700 AACCTAACAAAGAGC :: :: :: AAGATAATGCAGGA
1570 CAGAGGAGA ::::: TGGAGGGGT 990	1630 CATCTATAG : : AAAGTCGTC	1690 STACACAACC' : :: \TGGGGAAGA'
1550 1560 1570 TTGGTTCTACTGAGTGGGCAGAGGAAA :::::::::::::::X TTGGTCCGACTGAGTGGCTGGAGGGGTAC TTGGTCCGACTGAGTGGCTGGAGGGGTAC	10 1620 TTAATGCTGACT :::::::::::::::::::::::::::::::::::	1670 1680 TGATGTACAGCTTGG TATTATATACACTTA
1550 CTTGGT7 ::::: GTTGGT(1610 GCTTATATTAAT ::::::::: ACTTACATTAAT 1030	ACCGCTGATGTAC ::::::: CCCCCTATTATATATATATATATATATATATATATATAT
	CHEET (RULE 26)	pmsgen RATTRF

IGURE 16-8

		3	1/4	48		
) ; ; ; ; ;	TGAGGAACTTT	1190	1830	TGAGGTGTTCT	AGTTTCTTTCT	1250
	TTAGCAAAAT	1180	1820	GAAATGATTT	GAATCCCAGC	1240
	AGTAATTGGA	1170	1810	TTGGGATCTG	GCATATTCAG	1230
	ATATCGAAAC	1160	1800	GATAAGCAAA	CCCTTTTCTT	1220
	GAAAATATCT	1150	1790	GCATGCCCAG	ATGCTGCATT	1210
• • • • • • • • • • • • • • • • • • • •	ı	1140	1780	AGTTCAGTG	CCTTGGACA	1200
	2 RATTRF	ID CTITI				
			RATTRFTTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT 1140 1150 1160 1170 1180	RATTRFTTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGGAACTTT	-	RATTRFTTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTTT 1140 1150 1160 1170 1180 1190 1190 1820 1830 1830 1830 184 AGTTCAGTGCCAGGATAAGCAAATTGGGATCTGGAAATGATTTGAGGTGTTCTTTTTTTT

pmsgen ccgccactcarccrrrccrccrcarccrcacact-ccaccccrcacact

1420

1430

HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA

HUMTFR CATCTTTGGAGTTATTAAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGGCCCA

1280

1270

1260

1400

1300

IGURE 16-9

266 145 145 Human transferrin receptor mRNA, complete cd identity in 464 nt overlap 54.3% HUMTFRR

	ACAC	CCTC		1330	ACAA	••	LTAA		1390
	TTCL	: GTAA(H	ATTI	••	ATTC		<u>-</u>
1270	pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC	HUMTER TATGGAAGGAGACTGTCCCTCTGAAAAAAAACAGACTCTACATGTAGGATGGTAACCTC	1190	1320	pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATGAAGTGACAAGAATTTACAA	•••	HUMTFR AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGAGATAAAAATTCTTAA	1250	1380
	-TGG	ATGT		Ä	AGTG	••	AGAG		_
260	TTTAC	TCTAC	1180		A	••	CTGAA	1240	7.0
-	TGGC	AGAC			91\	••	\TGTG		1370
50	GGACC	AAAA	1170	1310	ACCA	•••	AGCA	1230	
12	ATGTT	ACTGG	٠.		CTCT-	••	CTGTG		1360
1240 1250 1260	CTACA	CTCTG	1160	1300	TC-CA	••••••••••••••	GCTCA	1220	c
12	STECC	rgtcc	**	-, , »	SCACA	•	STGAA		1350
1230	CAAAC	AGACT	1150	06	AGATO	••	GAATC	1210	1340
123	AGTCT	GAAGG	-	1290	AGTCA	••	AGCAA	-	1340
٠. ٠	AGGA	TATG	1140	0	AAAA	•••	AGAA	1200	. •
	nsgen	JMTFR	.T	1280	ısgen		IMTFR	12	
	ď	H		•		STIT			EET (1

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		,,	
pmsgen AAATTGTGAGGAGCTTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAACAA :::::::::::::::::::::::::::::	pmsgen TTTTGTTTGCAAGCTGGGATGCAGAATTTGGTCTTCTTGTTCTACTGAGTGGCAG ::::::::::::::::::::::::::::::::::	1570 1580 1590 1600 1610 1620 pmsgen A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCT :::::::::::::::::::::::::::::::	1630 1640 1650 1660 1670 1680 n ATAGAAGGAAACTACACTCTGAGGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC : ::::::::::::::::::::::::::::::::::
pmsg€ HUMTF			pmsgen HUMTFR
	SUBSTITUTE SH	FFT (RIH F 26)	

FIGURE 16-11

pmsgen	ACAACCTA	ACAAAAGAG	TGAAAAGCCC	TGATGAAGGC	1/30 FTTGAAGGCA	ACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG	
``	••	••					
HUMTFR	AAAACAATGCAAAATG	GCAAAATGT	GAAGCATCCGG	TTACTGGGCA	ATTTCTATAT	rgtgaagca tccggttactgggcaatttctatatcaggacagcaac	
	1620	1630	1640	1650	1660	1670	

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35/48 **FIGURE 17A**

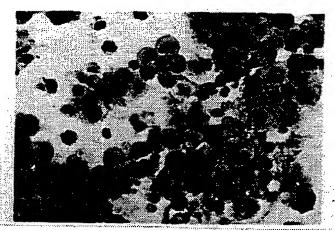


FIGURE 17B

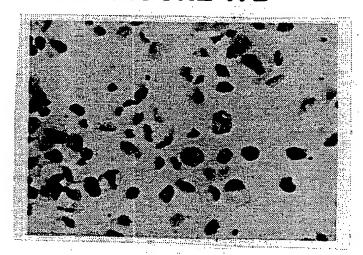
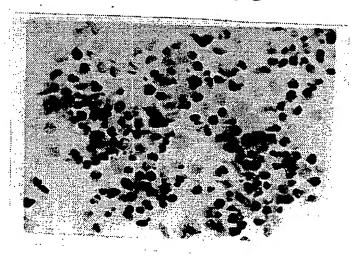


FIGURE 17C



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FIGURE 18

1 2 100 – 100 68 – 43 – 37/48

FIGURE 19

1 2 3 4

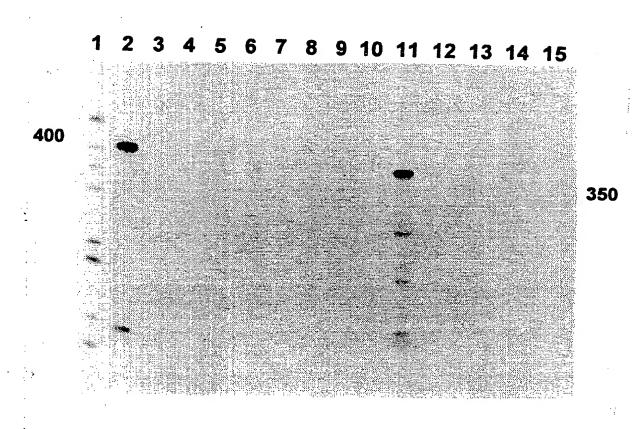
200 kDa ----

100 kDa ---

69 kDa ----

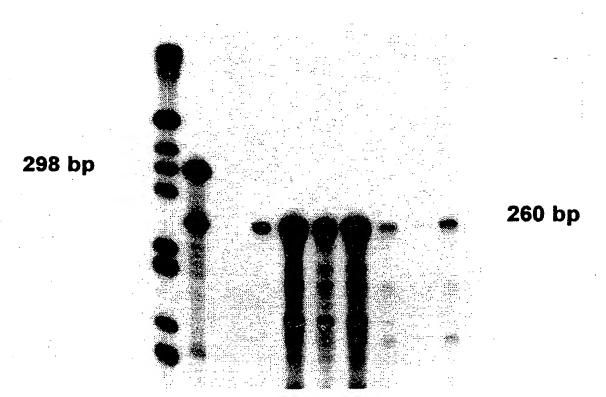
--- PSM

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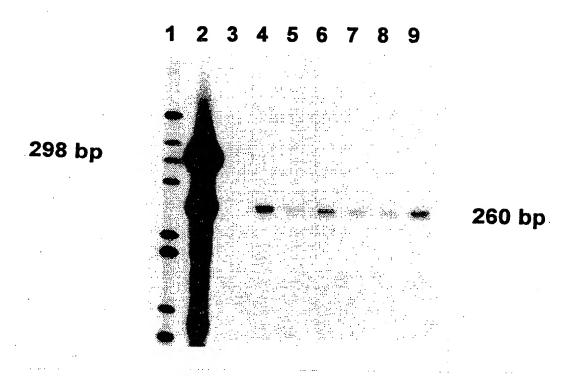


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1 2 3 4 5 6 7 8 9 10

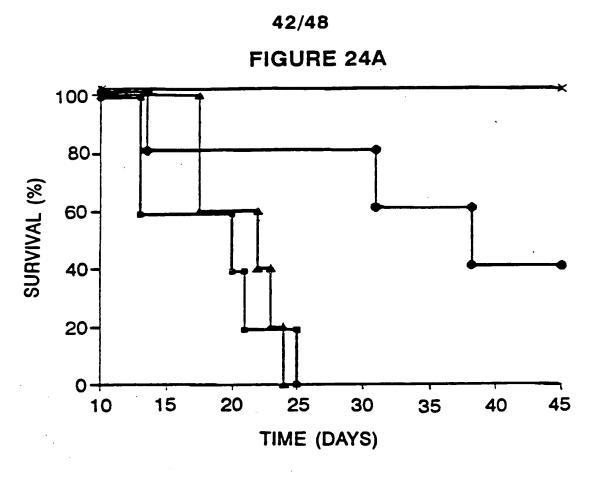


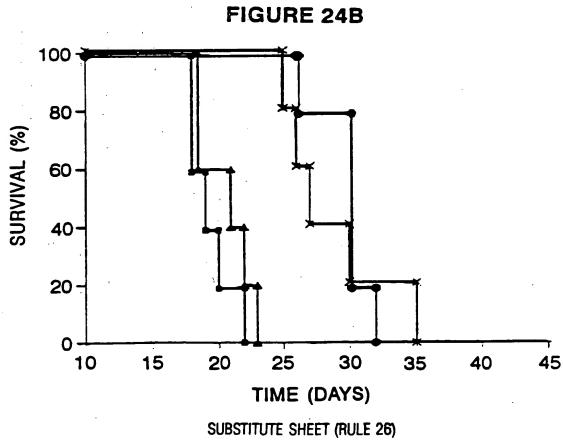
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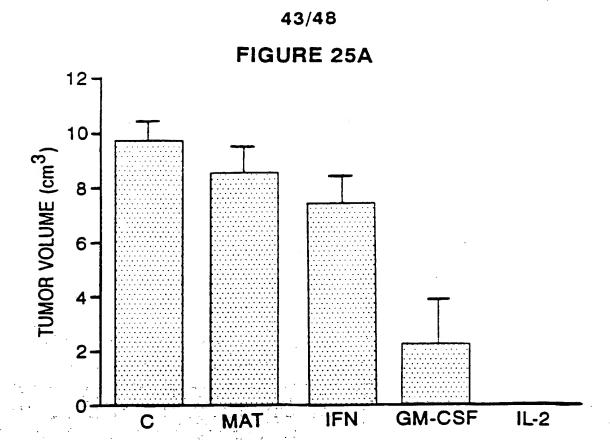


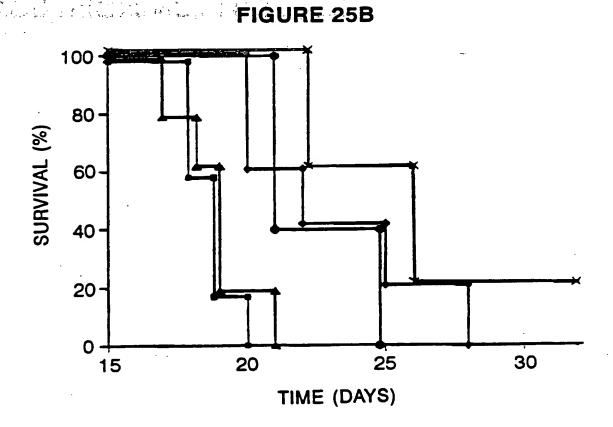
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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	· -	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES		-
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	_	ND
R1564-11-c12	YES	YES	ND	+



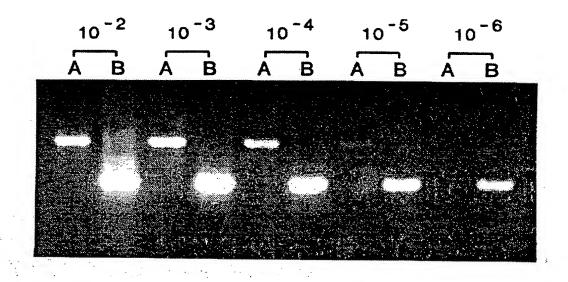






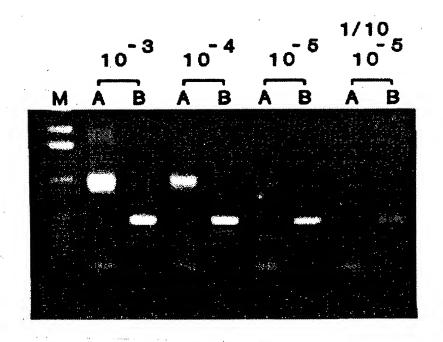
SUBSTITUTE SHEET (RULE 26)

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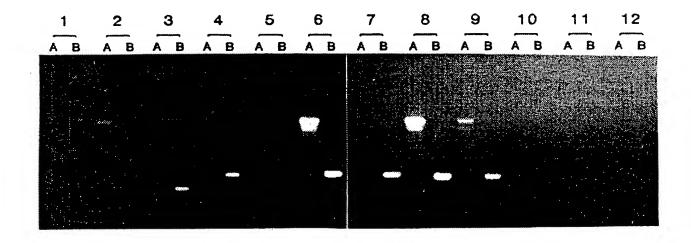


PCT/US93/10624

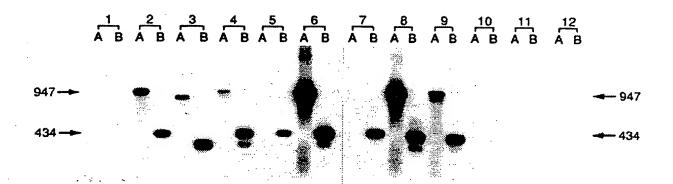
45/48

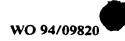


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Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR		
1	T2NxMo	None	8.9	0.7	_	+		
2	T2NoMo	RRP 7/93	6.1	_	_	+		
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+		
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+		
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+		
., v 6	Recur T3	I-125 1986	54.7	1.4	-	+		
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+		
8	T3NxMo	XRT 1987	7.5	0.1	_	-		
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-		
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	` +	+		
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+		
12	T2NoMo	RRP 8/91	NMA	0.5	_	+		
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-		
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	_		
15	D1	Proscar + Flutamide	20.8	0.5	-			
16	T2CNoMo	RRP 4/92	0.1	0.3		-		
SUBSTITUTE SHEET (RULE 26)								